



SEQUENCE LISTING

<110> Wands, Jack R.  
de la Monte, Suzanne M.  
Ince, Nedim  
Carlson, Rolf I.

<120> DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS

<130> 21486-032 DIV3

<140> 09/903,063  
<141> 2001-07-11

<150> 09/436,184  
<151> 1999-11-08

<160> 9

<170> PatentIn Ver. 2.1

<210> 1  
<211> 36  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Consensus  
EGF-like domain

<220>  
<221> VARIANT  
<222> (2)..(8)  
<223> Wherein Xaa is any amino acid

<220>  
<221> VARIANT  
<222> (10)..(13)  
<223> Wherein Xaa is any amino acid.

<220>  
<221> VARIANT  
<222> (15)..(24)  
<223> Wherein Xaa is any amino acid.

<220>  
<221> VARIANT  
<222> (26)

<223> Wherein Xaa is any amino acid.

<220>

<221> VARIANT

<222> (28)..(35)

<223> Wherein Xaa is any amino acid.

<400> 1

Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Cys Xaa Xaa  
1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Cys Xaa Xaa Xaa Xaa Xaa  
20 25 30

Xaa Xaa Xaa Cys  
35

<210> 2

<211> 758

<212> PRT

<213> Homo sapiens

<400> 2

Met Ala Gln Arg Lys Asn Ala Lys Ser Ser Gly Asn Ser Ser Ser Ser  
1 5 10 15

Gly Ser Gly Ser Gly Ser Thr Ser Ala Gly Ser Ser Ser Pro Gly Ala  
20 25 30

Arg Arg Glu Thr Lys His Gly Gly His Lys Asn Gly Arg Lys Gly Gly  
35 40 45

Leu Ser Gly Thr Ser Phe Phe Thr Trp Phe Met Val Ile Ala Leu Leu  
50 55 60

Gly Val Trp Thr Ser Val Ala Val Val Trp Phe Asp Leu Val Asp Tyr  
65 70 75 80

Glu Glu Val Leu Gly Lys Leu Gly Ile Tyr Asp Ala Asp Gly Asp Gly  
85 90 95

Asp Phe Asp Val Asp Asp Ala Lys Val Leu Leu Gly Leu Lys Glu Arg  
100 105 110

Ser Thr Ser Glu Pro Ala Val Pro Pro Glu Glu Ala Glu Pro His Thr  
115 120 125

Glu Pro Glu Glu Gln Val	Pro Val Glu Ala Glu Pro Gln Asn Ile Glu
130	135 140
Asp Glu Ala Lys Glu Gln Ile Gln Ser Leu Leu His Glu Met Val His	
145	150 155 160
Ala Glu His Val Glu Gly Glu Asp Leu Gln Gln Glu Asp Gly Pro Thr	
165	170 175
Gly Glu Pro Gln Gln Glu Asp Asp Glu Phe Leu Met Ala Thr Asp Val	
180	185 190
Asp Asp Arg Phe Glu Thr Leu Glu Pro Glu Val Ser His Glu Glu Thr	
195	200 205
Glu His Ser Tyr His Val Glu Glu Thr Val Ser Gln Asp Cys Asn Gln	
210	215 220
Asp Met Glu Glu Met Met Ser Glu Gln Glu Asn Pro Asp Ser Ser Glu	
225	230 235 240
Pro Val Val Glu Asp Glu Arg Leu His His Asp Thr Asp Asp Val Thr	
245	250 255
Tyr Gln Val Tyr Glu Glu Gln Ala Val Tyr Glu Pro Leu Glu Asn Glu	
260	265 270
Gly Ile Glu Ile Thr Glu Val Thr Ala Pro Pro Glu Asp Asn Pro Val	
275	280 285
Glu Asp Ser Gln Val Ile Val Glu Glu Val Ser Ile Phe Pro Val Glu	
290	295 300
Glu Gln Gln Glu Val Pro Pro Glu Thr Asn Arg Lys Thr Asp Asp Pro	
305	310 315 320
Glu Gln Lys Ala Lys Val Lys Lys Lys Lys Pro Lys Leu Leu Asn Lys	
325	330 335
Phe Asp Lys Thr Ile Lys Ala Glu Leu Asp Ala Ala Glu Lys Leu Arg	
340	345 350
Lys Arg Gly Lys Ile Glu Glu Ala Val Asn Ala Phe Lys Glu Leu Val	
355	360 365
Arg Lys Tyr Pro Gln Ser Pro Arg Ala Arg Tyr Gly Lys Ala Gln Cys	
370	375 380

Glu Asp Asp Leu Ala Glu Lys Arg Arg Ser Asn Glu Val Leu Arg Gly			
385	390	395	400
Ala Ile Glu Thr Tyr Gln Glu Val Ala Ser Leu Pro Asp Val Pro Ala			
	405	410	415
Asp Leu Leu Lys Leu Ser Leu Lys Arg Arg Ser Asp Arg Gln Gln Phe			
	420	425	430
Leu Gly His Met Arg Gly Ser Leu Leu Thr Leu Gln Arg Leu Val Gln			
	435	440	445
Leu Phe Pro Asn Asp Thr Ser Leu Lys Asn Asp Leu Gly Val Gly Tyr			
	450	455	460
Leu Leu Ile Gly Asp Asn Asp Asn Ala Lys Lys Val Tyr Glu Glu Val			
	465	470	475
		480	
Leu Ser Val Thr Pro Asn Asp Gly Phe Ala Lys Val His Tyr Gly Phe			
	485	490	495
Ile Leu Lys Ala Gln Asn Lys Ile Ala Glu Ser Ile Pro Tyr Leu Lys			
	500	505	510
Glu Gly Ile Glu Ser Gly Asp Pro Gly Thr Asp Asp Gly Arg Phe Tyr			
	515	520	525
Phe His Leu Gly Asp Ala Met Gln Arg Val Gly Asn Lys Glu Ala Tyr			
	530	535	540
Lys Trp Tyr Glu Leu Gly His Lys Arg Gly His Phe Ala Ser Val Trp			
	545	550	555
		560	
Gln Arg Ser Leu Tyr Asn Val Asn Gly Leu Lys Ala Gln Pro Trp Trp			
	565	570	575
Thr Pro Lys Glu Thr Gly Tyr Thr Glu Leu Val Lys Ser Leu Glu Arg			
	580	585	590
Asn Trp Lys Leu Ile Arg Asp Glu Gly Leu Ala Val Met Asp Lys Ala			
	595	600	605
Lys Gly Leu Phe Leu Pro Glu Asp Glu Asn Leu Arg Glu Lys Gly Asp			
	610	615	620
Trp Ser Gln Phe Thr Leu Trp Gln Gln Gly Arg Arg Asn Glu Asn Ala			
	625	630	635
		640	

Cys Lys Gly Ala Pro Lys Thr Cys Thr Leu Leu Glu Lys Phe Pro Glu  
645 650 655

Thr Thr Gly Cys Arg Arg Gly Gln Ile Lys Tyr Ser Ile Met His Pro  
660 665 670

Gly Thr His Val Trp Pro His Thr Gly Pro Thr Asn Cys Arg Leu Arg  
675 680 685

Met His Leu Gly Leu Val Ile Pro Lys Glu Gly Cys Lys Ile Arg Cys  
690 695 700

Ala Asn Glu Thr Arg Thr Trp Glu Glu Gly Lys Val Leu Ile Phe Asp  
705 710 715 720

Asp Ser Phe Glu His Glu Val Trp Gln Asp Ala Ser Ser Phe Arg Leu  
725 730 735

Ile Phe Ile Val Asp Val Trp His Pro Glu Leu Thr Pro Gln Gln Arg  
740 745 750

Arg Ser Leu Pro Ala Ile  
755

<210> 3

<211> 2324

<212> DNA

<213> Homo sapiens

<400> 3

cggaccgtgc aatggccag cgtaagaatg ccaagagcag cggcaacagc agcagcagcg 60  
gctccggcag cggtagcacg agtgcgggca gcagcagccc cggggcccg agagagacaa 120  
agcatggagg acacaagaat gggaggaaag gcggactctc gggaacttca ttcttcacgt 180  
ggtttatggt gattgcattg ctgggcgtct ggacatctgt agctgtcgtt tggtttgatc 240  
ttgttgacta tgaggaagtt ctaggaaaac taggaatcta tgatgctgat ggtgatggag 300  
atthttagtg ggatgatgcc aaagtthtat taggacttaa agagagatct acttcagagc 360  
cagcagtccc gccagaagag gctgagccac aactgagcc cgaggagcag gttcctgtgg 420  
aggcagaacc ccagaatatc gaagatgaag caaaagaaca aattcagtc cttctccatg 480  
aaatggtaca cgcagaacat gttgaggag aagacttgca acaagaagat ggaccacag 540  
gagaaccaca acaagaggat gatgagttt ttatggcgac tgatgtagat gatagatttg 600  
agaccctgga acctgaagta tctcatgaag aaaccgagca tagttaccac gtggaagaga 660  
cagtttcaca agactgtaat caggatatgg aagagatgat gtctgagcag gaaaatccag 720  
attccagtga accagtagta gaagatgaaa gattgcacca tgatacagat gatgtaacat 780  
accaagtcta tgaggaacaa gcagtatatg aacctctaga aatgaagg atagaaatca 840  
cagaagtaac tgctccccct gaggataatc ctgtagaaga ttcacaggta attgtagaag 900  
aagtaagcat ttttctgtg gaagaacagc aggaagtacc accagaaaca aatagaaaaa 960  
cagatgatcc agaacaaaaa gcaaaagtta agaaaaagaa gcctaaactt ttaaataaat 1020

```

ttgataagac tattaaagct gaacttgatg ctgcagaaaa actccgtaaa aggggaaaaa 1080
ttgaggaagc agtgaatgca tttaaagaac tagtacgcaa ataccctcag agtccacgag 1140
caagatatgg gaaggcgagc tgtgaggatg atttggctga gaagaggaga agtaatgagg 1200
tgctacgtgg agccatcgag acctaccaag aggtggccag cctacctgat gtccctgcag 1260
acctgctgaa gctgagtttg aagcgctcgt cagacaggca acaatttcta ggcatatga 1320
gaggttccct gcttaccctg cagagattag ttcaactatt tcccaatgat acttccttaa 1380
aaaatgacct tggcgtggga tacctcttga taggagataa tgacaatgca aagaaagttt 1440
atgaagaggt gctgagtgtg acacctaata atggctttgc taaagtccat tatggcttca 1500
tctgaaggc acagaacaaa attgctgaga gcacccata tttaaaggaa ggaatagaat 1560
ccggagatcc tggcactgat gatgggagat tttatttcca cctgggggat gccatgcaga 1620
gggttgggaa caaagaggca tataagtggg atgagcttgg gcacaagaga ggacactttg 1680
catctgtctg gcaacgctca ctctacaatg tgaatggact gaaagcacag ccttgggtgga 1740
cccaaaaaga aacgggctac acagagttag taaagtcttt agaaagaaac tggaagttaa 1800
tccgagatga aggccttgca gtgatggata aagccaaagg tctcttcctg cctgaggatg 1860
aaaacctgag ggaaaaaggg gactggagcc agttcacgct gtggcagcaa ggaagaagaa 1920
atgaaaatgc ctgcaaagga gctcctaaaa cctgtacctt actagaaaag ttccccgaga 1980
caacaggatg cagaagagga cagatcaaat attccatcat gcaccccgag actcacgtgt 2040
ggccgcacac agggcccaca aactgcaggc tccgaatgca cctgggcttg gtgattccca 2100
aggaaggctg caagattcga tgtgccaacg agaccaggac ctgggaggaa ggcaagggtg 2160
tcatctttga tgactccttt gagcacgagg tatggcagga tgctcatct ttccggctga 2220
tattcatcgt ggatgtgtgg catccggaac tgacaccaca gcagagacgc agccttccag 2280
caatttagca tgaattcatg caagcttggg aaactctgga gaga 2324

```

<210> 4

<211> 31

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: EGF-like  
cysteine-rich repeat

<220>

<221> VARIANT

<222> (3)..(5)

<223> Wherein any Xaa may be any amino acid

<220>

<221> VARIANT

<222> (6)..(7)

<223> Wherein Xaa is any amino acid.

<220>

<221> VARIANT

<222> (10)

<223> Wherein Xaa is any amino acid.

<220>  
 <221> VARIANT  
 <222> (14)  
 <223> Wherein Xaa is any amino acid.

<220>  
 <221> VARIANT  
 <222> (17)..(18)

<220>  
 <221> VARIANT  
 <222> (25)..(26)  
 <223> Wherein Xaa is any amino acid.

<220>  
 <221> VARIANT  
 <222> (29)  
 <223> Wherein Xaa is any amino acid.

<400> 4  
 Cys Asp Xaa Xaa Xaa Cys Xaa Xaa Lys Xaa Gly Asn Gly Xaa Cys Asp  
           1                  5                  10                  15  
 Xaa Xaa Cys Asn Asn Ala Ala Cys Xaa Xaa Asp Gly Xaa Asp Cys  
                   20                  25                  30

<210> 5  
 <211> 1242  
 <212> PRT  
 <213> Homo sapiens

<400> 5  
 Met Ala Ser Pro Pro Glu Ser Asp Gly Phe Ser Asp Val Arg Lys Val  
           1                  5                  10                  15  
 Gly Tyr Leu Arg Lys Pro Lys Ser Met His Lys Arg Phe Phe Val Leu  
                   20                  25                  30  
 Arg Ala Ala Ser Glu Ala Gly Gly Pro Ala Arg Leu Glu Tyr Tyr Glu  
                   35                  40                  45  
 Asn Glu Lys Lys Trp Arg His Lys Ser Ser Ala Pro Lys Arg Ser Ile  
           50                  55                  60  
 Pro Leu Glu Ser Cys Phe Asn Ile Asn Lys Arg Ala Asp Ser Lys Asn  
           65                  70                  75                  80

Lys His Leu Val Ala Leu Tyr Thr Arg Asp Glu His Phe Ala Ile Ala  
                     85                    90                    95

Ala Asp Ser Glu Ala Glu Gln Asp Ser Trp Tyr Gln Ala Leu Leu Gln  
                     100                    105                    110

Leu His Asn Arg Ala Lys Gly His His Asp Gly Ala Ala Ala Leu Gly  
                     115                    120                    125

Ala Gly Gly Gly Gly Gly Ser Cys Ser Gly Ser Ser Gly Leu Gly Glu  
                     130                    135                    140

Ala Gly Glu Asp Leu Ser Tyr Gly Asp Val Pro Pro Gly Pro Ala Phe  
 145                    150                    155                    160

Lys Glu Val Trp Gln Val Ile Leu Lys Pro Lys Gly Leu Gly Gln Thr  
                     165                    170                    175

Lys Asn Leu Ile Gly Ile Tyr Arg Leu Cys Leu Thr Ser Lys Thr Ile  
                     180                    185                    190

Ser Phe Val Lys Leu Asn Ser Glu Ala Ala Ala Val Val Leu Gln Leu  
                     195                    200                    205

Met Asn Ile Arg Arg Cys Gly His Ser Glu Asn Phe Phe Phe Ile Glu  
                     210                    215                    220

Val Gly Arg Ser Ala Val Thr Gly Pro Gly Glu Phe Trp Met Gln Val  
 225                    230                    235                    240

Asp Asp Ser Val Val Ala Gln Asn Met His Glu Thr Ile Leu Glu Ala  
                     245                    250                    255

Met Arg Ala Met Ser Asp Glu Phe Arg Pro Arg Ser Lys Ser Gln Ser  
                     260                    265                    270

Ser Ser Asn Cys Ser Asn Pro Ile Ser Val Pro Leu Arg Arg His His  
                     275                    280                    285

Leu Asn Asn Pro Pro Pro Ser Gln Val Gly Leu Thr Arg Arg Ser Arg  
                     290                    295                    300

Thr Glu Ser Ile Thr Ala Thr Ser Pro Ala Ser Met Val Gly Gly Lys  
 305                    310                    315                    320

Pro Gly Ser Phe Arg Val Arg Ala Ser Ser Asp Gly Glu Gly Thr Met  
                     325                    330                    335



Ser Arg Pro Ala Ser Val Asp Gly Ser Pro Val Ser Pro Ser Thr Asn  
 340 345 350

Arg Thr His Ala His Arg His Arg Gly Ser Ala Arg Leu His Pro Pro  
 355 360 365

Leu Asn His Ser Arg Ser Ile Pro Met Pro Ala Ser Arg Cys Ser Pro  
 370 375 380

Ser Ala Thr Ser Pro Val Ser Leu Ser Ser Ser Thr Ser Gly His  
 385 390 395 400

Gly Ser Thr Ser Asp Cys Leu Phe Pro Arg Arg Ser Ser Ala Ser Val  
 405 410 415

Ser Gly Ser Pro Ser Asp Gly Gly Phe Ile Ser Ser Asp Glu Tyr Gly  
 420 425 430

Ser Ser Pro Cys Asp Phe Arg Ser Ser Phe Arg Ser Val Thr Pro Asp  
 435 440 445

Ser Leu Gly His Thr Pro Pro Ala Arg Gly Glu Glu Glu Leu Ser Asn  
 450 455 460

Tyr Ile Cys Met Gly Gly Lys Gly Pro Ser Thr Leu Thr Ala Pro Asn  
 465 470 475 480

Gly His Tyr Ile Leu Ser Arg Gly Gly Asn Gly His Arg Cys Thr Pro  
 485 490 495

Gly Thr Gly Leu Gly Thr Ser Pro Ala Leu Ala Gly Asp Glu Ala Ala  
 500 505 510

Ser Ala Ala Asp Leu Asp Asn Arg Phe Arg Lys Arg Thr His Ser Ala  
 515 520 525

Gly Thr Ser Pro Thr Ile Thr His Gln Lys Thr Pro Ser Gln Ser Ser  
 530 535 540

Val Ala Ser Ile Glu Glu Tyr Thr Glu Met Met Pro Ala Tyr Pro Pro  
 545 550 555 560

Gly Gly Gly Ser Gly Gly Arg Leu Pro Gly His Arg His Ser Ala Phe  
 565 570 575

Val Pro Thr Arg Ser Tyr Pro Glu Glu Gly Leu Glu Met His Pro Leu  
 580 585 590

Glu	Arg	Arg	Gly	Gly	His	His	Arg	Pro	Asp	Ser	Ser	Thr	Leu	His	Thr	595	600	605	
Asp	Asp	Gly	Tyr	Met	Pro	Met	Ser	Pro	Gly	Val	Ala	Pro	Val	Pro	Ser	610	615	620	
Gly	Arg	Lys	Gly	Ser	Gly	Asp	Tyr	Met	Pro	Met	Ser	Pro	Lys	Ser	Val	625	630	635	640
Ser	Ala	Pro	Gln	Gln	Ile	Ile	Asn	Pro	Ile	Arg	Arg	His	Pro	Gln	Arg	645	650	655	
Val	Asp	Pro	Asn	Gly	Tyr	Met	Met	Met	Ser	Pro	Ser	Gly	Gly	Cys	Ser	660	665	670	
Pro	Asp	Ile	Gly	Gly	Gly	Pro	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Asn	Ala	675	680	685	
Val	Pro	Ser	Gly	Thr	Ser	Tyr	Gly	Lys	Leu	Trp	Thr	Asn	Gly	Val	Gly	690	695	700	
Gly	His	His	Ser	His	Val	Leu	Pro	His	Pro	Lys	Pro	Pro	Val	Glu	Ser	705	710	715	720
Ser	Gly	Gly	Lys	Leu	Leu	Pro	Cys	Thr	Gly	Asp	Tyr	Met	Asn	Met	Ser	725	730	735	
Pro	Val	Gly	Asp	Ser	Asn	Thr	Ser	Ser	Pro	Ser	Asp	Cys	Tyr	Tyr	Gly	740	745	750	
Pro	Glu	Asp	Pro	Gln	His	Lys	Pro	Val	Leu	Ser	Tyr	Tyr	Ser	Leu	Pro	755	760	765	
Arg	Ser	Phe	Lys	His	Thr	Gln	Arg	Pro	Gly	Glu	Pro	Glu	Glu	Gly	Ala	770	775	780	
Arg	His	Gln	His	Leu	Arg	Leu	Ser	Thr	Ser	Ser	Gly	Arg	Leu	Leu	Tyr	785	790	795	800
Ala	Ala	Thr	Ala	Asp	Asp	Ser	Ser	Ser	Ser	Thr	Ser	Ser	Asp	Ser	Leu	805	810	815	
Gly	Gly	Gly	Tyr	Cys	Gly	Ala	Arg	Leu	Glu	Pro	Ser	Leu	Pro	His	Pro	820	825	830	
His	His	Gln	Val	Leu	Gln	Pro	His	Leu	Pro	Arg	Lys	Val	Asp	Thr	Ala	835	840	845	

Ala Gln Thr Asn Ser Arg Leu Ala Arg Pro Thr Arg Leu Ser Leu Gly  
 850 855 860

Asp Pro Lys Ala Ser Thr Leu Pro Arg Ala Arg Glu Gln Gln Gln Gln  
 865 870 875 880

Gln Gln Pro Leu Leu His Pro Pro Glu Pro Lys Ser Pro Gly Glu Tyr  
 885 890 895

Val Asn Ile Glu Phe Gly Ser Asp Gln Ser Gly Tyr Leu Ser Gly Pro  
 900 905 910

Val Ala Phe His Ser Ser Pro Ser Val Arg Cys Pro Ser Gln Leu Gln  
 915 920 925

Pro Ala Pro Arg Glu Glu Glu Thr Gly Thr Glu Glu Tyr Met Lys Met  
 930 935 940

Asp Leu Gly Pro Gly Arg Arg Ala Ala Trp Gln Glu Ser Thr Gly Val  
 945 950 955 960

Glu Met Gly Arg Leu Gly Pro Ala Pro Pro Gly Ala Ala Ser Ile Cys  
 965 970 975

Arg Pro Thr Arg Ala Val Pro Ser Ser Arg Gly Asp Tyr Met Thr Met  
 980 985 990

Gln Met Ser Cys Pro Arg Gln Ser Tyr Val Asp Thr Ser Pro Ala Ala  
 995 1000 1005

Pro Val Ser Tyr Ala Asp Met Arg Thr Gly Ile Ala Ala Glu Glu Val  
 1010 1015 1020

Ser Leu Pro Arg Ala Thr Met Ala Ala Ala Ser Ser Ser Ser Ala Ala  
 1025 1030 1035 1040

Ser Ala Ser Pro Thr Gly Pro Gln Gly Ala Ala Glu Leu Ala Ala His  
 1045 1050 1055

Ser Ser Leu Leu Gly Gly Pro Gln Gly Pro Gly Gly Met Ser Ala Phe  
 1060 1065 1070

Thr Arg Val Asn Leu Ser Pro Asn Arg Asn Gln Ser Ala Lys Val Ile  
 1075 1080 1085

Arg Ala Asp Pro Gln Gly Cys Arg Arg Arg His Ser Ser Glu Thr Phe  
 1090 1095 1100

Ser Ser Thr Pro Ser Ala Thr Arg Val Gly Asn Thr Val Pro Phe Gly  
 1105 1110 1115 1120

Ala Gly Ala Ala Val Gly Gly Gly Gly Ser Ser Ser Ser Ser Glu  
 1125 1130 1135

Asp Val Lys Arg His Ser Ser Ala Ser Phe Glu Asn Val Trp Leu Arg  
 1140 1145 1150

Pro Gly Glu Leu Gly Gly Ala Pro Lys Glu Pro Ala Lys Leu Cys Gly  
 1155 1160 1165

Ala Ala Gly Gly Leu Glu Asn Gly Leu Asn Tyr Ile Asp Leu Asp Leu  
 1170 1175 1180

Val Lys Asp Phe Lys Gln Cys Pro Gln Glu Cys Thr Pro Glu Pro Gln  
 1185 1190 1195 1200

Pro Pro Pro Pro Pro Pro Pro His Gln Pro Leu Gly Ser Gly Glu Ser  
 1205 1210 1215

Ser Ser Thr Arg Arg Ser Ser Glu Asp Leu Ser Ala Tyr Ala Ser Ile  
 1220 1225 1230

Ser Phe Gln Lys Gln Pro Glu Asp Arg Gln  
 1235 1240

<210> 6  
 <211> 5828  
 <212> DNA  
 <213> Homo sapiens

<400> 6  
 cgggcgcgcg gtcggagggg gccggcgcgcg agagccagac gccgcccgtt gttttggttg 60  
 gggctctcgg caactctccg aggaggagga ggaggaggga ggaggggaga agtaactgca 120  
 gcggcagcgc cctcccgagg aacaggcgtc ttccccgaac ccttcccaaa cctcccccat 180  
 cccctctcgc cttgtcccc tccctctctc ccagccgcc tggagcgagg ggcagggatg 240  
 agtctgtccc tccggccggt cccagctgc agtggtgcc cggtatcggt tcgcatggaa 300  
 aagccacttt ctccaccgc cgagatgggc ccgatgggg ctgcagagga cgcgcccgcg 360  
 ggcggcggca gcagcagcag cagcagcagc agcaacagca acagccgcag cgcgcgggtc 420  
 tctgcgactg agctggtatt tgggcggctg gtggcggctg ggacggttg ggggtgggag 480  
 gaggcgaagg aggagggaga accccgtgca acgttgggac ttggcaacct gcctccccct 540  
 gcccaggat atttaatttg cctcgggaat cgctgcttcc agaggggaac tcaggaggga 600  
 aggcgcgcgc gcgcgcgcgc tcttgagggg gcaccgcagg gacccccgac tgtcgctctc 660  
 ctgtgccgga ctccagccgg ggcgacgaga gatgcattct cgctccttcc tgggtggcggc 720  
 ggcggctgag aggagacttg gctctcggag gatcggggct gccctcacct cggacgcact 780  
 gcctccccgc cggcgtgaag cgcccgaaaa ctccggtcgg gctctctcct gggctcagca 840

gctgcgtcct	ccttcagctg	ccccccccg	gcgcgggggg	cggcgtggat	ttcagagtcg	900
gggtttctgc	tgcctccagc	cctgtttgca	tgtgccgggc	cgcggcgagg	agcctccgcc	960
ccccacccgg	ttgtttttcg	gagcctccct	ctgctcagcg	ttggtggtgg	cggtggcagc	1020
atggcgagcc	ctccggagag	cgatggcttc	tcgacgtgc	gcaaggtggg	ctacctgcgc	1080
aaacccaaga	gcatgcacaa	acgtttcttc	gtactgcgcg	cggccagcga	ggctggggggc	1140
ccggcgcgcc	tcgagtacta	cgagaacgag	aagaagtggc	ggcacaagtc	gagcgccccc	1200
aaacgctcga	ttcccccttg	gagctgcttc	aacatcaaca	agcgggctga	ctccaagaac	1260
aagcacctgg	tggctctcta	cacccgggac	gagcactttg	ccatcgcggc	ggacagcgag	1320
gccgagcaag	acagctggta	ccaggtcttc	ctacagctgc	acaaccgtgc	taagggccac	1380
cacgacggag	ctgcggccct	cggggcggga	ggtggtgggg	gcagctgcag	cggcagctcc	1440
ggccttggtg	aggctgggga	ggacttgagc	tacggtgacg	tgcccccagg	acccgcattc	1500
aaagaggtct	ggcaagtgat	cctgaagccc	aagggcctgg	gtcagacaaa	gaacctgatt	1560
ggtatctacc	gcctttgcct	gaccagcaag	accatcagct	tcgtgaagct	gaactcggag	1620
gcagcggccg	tgggtgctga	gctgatgaac	atcaggcgct	gtggccactc	ggaaaacttc	1680
ttcttcatcg	aggtgggccc	ttctgccgtg	acggggcccc	gggagttctg	gatgcagggtg	1740
gatgactctg	tgggtggccca	gaacatgcac	gagaccatcc	tggaggccat	gcggggccatg	1800
agtgatgagt	tccgcctctg	cagcaagagc	cagtcctcgt	ccaactgctc	taaccccatc	1860
agcgtccccc	tgcgcgggca	ccatctcaac	aatcccccg	ccagccaggt	ggggctgacc	1920
cgccgatcac	gcaactgagag	catcacgcgc	acctccccgg	ccagcatggt	gggcgggaag	1980
ccaggctcct	tccgtgtccg	cgcctccagt	gacggcgaag	gcaccatgtc	ccgcccagcc	2040
tcggtggacg	gcagccctgt	gagtcccagc	accaacagaa	cccacgccc	ccggcatcgg	2100
ggcagcggcc	ggctgcaccc	cccgtcaac	cacagccgct	ccatccccat	gccggcttcc	2160
cgctgctcgc	cttcggccac	cagcccggtc	agtctgtcgt	ccagtagcac	cagtggccat	2220
ggctccacct	cggattgtct	cttcccacgg	cgatctagt	cttcgggtgtc	tggttccccc	2280
agcgatggcg	gtttcatctc	ctcggatgag	tatggctcca	gtccctgcga	tttcgggagt	2340
tccttcgcga	gtgtcactcc	ggattccctg	ggccacaccc	caccagcccc	cggtagaggag	2400
gagctaagca	actatatctg	catgggtggc	aaggggccct	ccaccctgac	cgcccccaac	2460
ggtcactaca	ttttgtctcg	gggtggcaat	ggccaccgct	gcaccccagg	aacaggcttg	2520
ggcacgagtc	cagccttggc	tggggatgaa	gcagccagt	ctgcagatct	ggataatcgg	2580
ttccgaaaga	gaactcactc	ggcaggcaca	tccctacca	ttacccacca	gaagaccccg	2640
tcccagtcct	cagtggcttc	cattgaggag	tacacagaga	tgatgcctgc	ctacccacca	2700
ggaggtggca	gtggaggccg	actgccggga	cacaggcact	ccgccttcgt	gcccacccgc	2760
tcctacccag	aggagggtct	ggaaatgcac	cccttgaggc	gtcggggggg	gcaccaccgc	2820
ccagacagct	ccaccctcca	cacggatgat	ggctacatgc	ccatgtcccc	aggggtggcc	2880
ccagtgccca	gtggccgaaa	gggcagtggg	gactatatgc	ccatgagccc	caagagcgta	2940
tctgccccac	agcagatcat	caatcccatc	agacgccatc	cccagagagt	ggaccccaat	3000
ggctacatga	tgatgtcccc	cagcggtggc	tgtctcctg	acattggagg	tggcccccagc	3060
agcagcagca	gcagcagcaa	cgcgtccct	tccgggacca	gctatggaaa	gctgtggaca	3120
aacggggtag	ggggccacca	ctctcatgtc	ttgcctcacc	ccaaaccccc	agtggagagc	3180
agcgggtggt	agctcttacc	ttgcacaggt	gactacatga	acatgtcacc	agtggggggac	3240
tccaacacca	gcagcccctc	cgactgctac	tacggccctg	aggaccccca	gcacaagcca	3300
gtcctctcct	actactcatt	gccaagatcc	tttaagcaca	cccagcgccc	cggggagccg	3360
gaggaggggtg	cccggcatca	gcacctccgc	ctttccacta	gctctggtcg	ccttctctat	3420
gctgcaacag	cagatgattc	ttcctcttcc	accagcagcg	acagcctggg	tgggggatac	3480
tgcggggcta	ggctggagcc	cagccttcca	catccccacc	atcaggttct	gcagcccat	3540
ctgcctcgaa	aggtggacac	agctgctcag	accaatagcc	gcctggcccc	gcccacgagg	3600
ctgtccctgg	gggatcccaa	ggccagcacc	ttacctcggg	cccagagaca	gcagcagcag	3660
cagcagccct	tgctgcaccc	tccagagccc	aagagcccgg	gggaatatgt	caatattgaa	3720

```

tttgggagtg atcagttctgg ctacttgtct ggcccgggtgg ctttccacag ctcaccttct 3780
gtcagggtgtc catcccagct ccagccagct cccagagagg aagagactgg cactgaggag 3840
tacatgaaga tggacctggg gccggggccgg agggcagcct ggcaggagag cactgggggtc 3900
gagatggggca gactggggccc tgcacctccc ggggctgcta gcatttgcag gcctaccccg 3960
gcagtgtcca gcagccgggg tgactacatg accatgcaga tgagtgttcc ccgtcagagc 4020
tacgtggaca cctcgccagc tggccctgta agctatgctg acatgcgaac aggcattgct 4080
gcagaggagg tgagcctgcc cagggccacc atggctgctg cctcctcatc ctcagcagcc 4140
tctgcttccc cgactggggc tcaaggggca gcagagctgg ctgcccactc gtccctgctg 4200
ggggggccac aaggacctgg gggcatgagc gccttcaccc gggtgaaact cagtccctaac 4260
cgcaaccaga gtgccaaagt gatccgtgca gaccacaag ggtgccggcg gaggcatagc 4320
tccgagactt tctcctcaac acccagtgcc acccgggtgg gcaacacagt gccctttgga 4380
gcgggggagc cagtaggggg cgggtggcgg agcagcagca gcagcgagga tgtgaaacgc 4440
cacagctctg cttcctttga gaatgtgtgg ctgaggcctg gggagcttgg gggagcccc 4500
aaggagccag ccaaactgtg tggggctgct gggggtttgg agaattgtct taactacata 4560
gacctggatt tgggtcaagga cttcaaacag tgccctcagg agtgcacccc tgaaccgcag 4620
cctccccac cccaccccc tcatcaaccc ctgggcagcg gtgagagcag ctccaccgcg 4680
cgctcaagtg aggatttaag cgcctatgcc agcatcagtt tccagaagca gccagaggac 4740
cgtcagtagc tcaactggac atcacagcag aatgaagacc taaatgacct cagcaaattc 4800
tcttctaact catgggtacc cagactctaa atatttcatg attcacaact aggacctcat 4860
atcttcctca tcagtagatg gtacgatgca tccatttcag tttgtttact ttatccaatc 4920
ctcaggattt cattgactga actgcacgtt ctatattgtg ccaagcgaaa aaaaaaatg 4980
cactgtgaca ccagaataat gagtctgcat aaacttcac ttcaacctta aggacttagc 5040
tggccacagt gagctgatgt gcccaccacc gtgtcatgag agaattgggtt tactctcaat 5100
gcattttcaa gatacatttc atctgctgct gaaactgtgt acgacaaagc atcattgtaa 5160
attatttcat acaaaactgt tcacgttggg tggagagagt attaaatatt taacataggt 5220
tttgatttat atgtgtaatt ttttaaataa aaatgtaact tttcttacag cacatctttt 5280
ttttggatgt gggatggagg tatacaatgt tctgttgtaa agagtggagc aaatgcttaa 5340
aacaaggctt aaaagagtag aatagggtat gatccttgtt ttaagattgt aattcagaaa 5400
acataatata agaatacatg tgccatagat ggttctcaat tgtatagtta ttttgctga 5460
tactatctct tgtcatataa acctgatgtt gagctgagtt ccttataaga attaatctta 5520
attttgtatt ttttctgtg agacaatagg ccatgttaat taaactgaag aaggatatat 5580
ttggctgggt gttttcaaat gtcagcttaa aattggtaat tgaatggaag caaaattata 5640
agaagaggaa attaaagtct tcattgcat gtattgtaaa cagaaggaga tgggtgattc 5700
cttcaattca aaagctctct ttggaatgaa caatgtgggc gtttgtaaat tctggaaatg 5760
tctttctatt cataataaac tagatactgt tgatctttta aaaaaaaaaa aaaaaaaaaa 5820
aaaaaaaaa

```

<210> 7

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: FLAG epitope

<400> 7

Asp Tyr Lys Asp Asp Asp Asp Lys

1

5

<210> 8

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer

<400> 8

gggggaattt gtcaata

17

<210> 9

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer

<400> 9

gaatttggtta atattg

16